7 Cookbook

7.1 Setting up the Environment

Create the directory for the analysis

```
mkdir jemx_data_rep
cd jemx_data_rep
setenv REP_BASE_PROD  $PWD
unsetenv AUXL_REF_DIR
```

Install there the test data, as it is explained in the Installation Guide for the *INTEGRAL* Data Analysis System [4]. The setting of the environment is explained in Section "Working Environment" of the Introduction to the *INTEGRAL* Data Analysis [1].

After the installation of the test data you find the RAW and PRP data (see Appendix A) with which you start the analysis under **scw** branch.

To have log messages both on the screen and in a file (**log** in the given example) give the command

```
setenv COMMONLOGFILE +log
```

If you don't want the GUI window to appear after you launch the analysis

```
setenv COMMONSCRIPT 1
```

7.2 Observation Group Creation

After setting up the environment you are ready to call the analysis script.

The first thing to do is to create a list of the Science Windows you want to analyze. The following example is based on the Crab observations. To follow it create ASCII file **jemx2.lst** with the list of DOL's of the prepared Science Window Groups you want to analyze. (DOL (Data Object Locator) specifies the Data Structure in the FITS file you are interested in, see more details in the Introduction to the *INTEGRAL* Data Analysis [1].)

```
scw/0102/010200210010.000/swg.fits[1]
scw/0102/010200220010.000/swg.fits[1]
```

Warning! Please note that there is different naming scheme for revision 1 and revision 2 data. For the revision 1 data the name of the prepared Science Window Group is `swg_prp.fits`.

Now you are ready to create an Observation Group (see the description of the executable *og_create* in the Toolbox section of the Introduction to the *INTEGRAL* Data Analysis [1]):

```
og_create idxSwg=jemx2.lst ogid=crab  baseDir="./" instrument=JMX2
```

This command creates the directory **obs/crab** in which all the results will be located and copy there all the data needed for the analysis.

Warning! In OSA 4.2 the structure of the results slightly differs from the previous versions. Directories **jmx1/**, **jmx2/** and **scw/RRRRPPPPSSSF.00V/jmx1/ scw/RRRRPPPPSSSF.00V/jmx2/** do not exist any more, see [1] for more details. Do not forget to update your scripts!

7.3 Examples on Image Creation

Now you are ready to change the directory and start the analysis. In the following examples we start with the building of the images of the sky region observed in the chosen Science Windows.

Do not forget that there are two JEMX instruments - JEMX 1 and JEMX 2. To define the instrument you are interested in set the parameter `jemxNum` to either 1 or 2. The default value is

```
jemxNum=2
```

In the Overview chapter you have seen that there are different levels of the script. You can choose to run only part of them. There are two parameters defining the start and end levels of the data to be analyzed (default values are given):

```
startLevel="CAT_I"
endLevel="IMA2"
```

If you are using revision 2 data then steps **COR, DEAD, GTI** were already processed for you at ISDC. Still all the executables necessary to rerun this job are available within the pipeline, see e.g. example on use of the user-defined GTIs in Section 7.6. If you use revision 1 data you have to start your analysis from the COR level.

To skip some levels use parameter `skipLevels` (default value is given below):

```
skipLevels="BKG,LCR,BIN_T"
```

Be careful while setting this parameter – levels often depend on the previous ones, so make sure that your selection makes sense. In all examples given here BKG level is skipped, as there are no realistic background models at the moment.

The energy range of the desired images can be chosen with the parameters of the main script. You should set the desired energy bands in channels. With the help of Table 3 you can choose those corresponding to the desired keV range.

Four default output energy bands are defined for JEM-X:

```
nChanBins=4               Number of channel bands
chanLow="46 83 129 160"   Lower channel boundaries
chanHigh="82 128 159 223" Upper channel boundaries
```

These ranges corresponds closely to 3 – 6 keV, 6 – 10 keV, 10 – 15 keV and 15 – 35 keV (see Table 3).

If you do not want software to find the position of the catalog sources, but to use the catalog values you should change the default value of the `IMA_useCatPos` parameter

```
IMA_useCatPos=y
```

7.3.1 Case 1: First Try

The command given below launches the analysis of the data attached to the just created Observation Group. The analysis will pass all the stages, except BKG, from Catalog source selection (CAT_I) to the Imaging level (IMA). At the beginning script launches the Graphic User Interface (GUI) and you have a chance to check the parameter settings (the full list of the parameters is

given in Table 6). Only non hidden parameters appear. To see hidden parameters press button "`hidden`", to close again the window with hidden parameters press "`Ok`". Note that if you leave parameter `og_dol` empty (default value) script will find the DOL of observational group on its own. When you are ready press "`Run`" to start the analysis.

In the Table 6 at the end of this Section we list all the parameters of the main script with a brief explanation. To mark queried parameters bold font has been used. The detailed description of the main script structure and algorithms is given in Section 8.

```
cd obs/crab
jemx_science_analysis startLevel="CAT_I" \
endLevel="IMA"  jemxNum=2 IMA_vignCorr=no
```

For the discussion on the parameter `IMA_vignCorr` see Case 4.

Here we discuss the results only briefly. For a more detailed discussion, see the Appendix. At this level all results are produced at Science Window level only. The output of the analysis is located at **scw/RRRRPPPPSSSF.000/** (RRRRPPPPSSSF is a number of the Science Window).

Go to one of these directories and have a look at files located there

```
cd scw/010200210010.000/
ls
```

There you can find an output from all the steps done by the script.

The output image is in the file **jmx2_sky_ima.fits** You can check with fv

```
fv jmx2_sky_ima.fits
```

that this file has four images inside (one image per selected energy band).

In the file **jmx2_srcl_res.fits** you find a list of all found sources, and in the file **jmx2_srcl_cat.fits** the list of the sources in the input catalog. You can see that most of the sources were not found, as they are too weak. When you run the lightcurve and spectra extraction steps the results would be produced for all found sources from **jmx2_srcl_res.fits**. You can also extract the result for any given position in the field of view. To do this you should use user catalog, as it is described in Section 7.7.

There is a nice way to locate the found sources on the sky image. To do it use the program **cat2ds9**.

```
cat2ds9 jmx2_srcl_res.fits\[1] found.reg symbol=box color=red
cat2ds9 jmx2_srcl_cat.fits\[1] cat.reg symbol=box color=white
```

To find more about this program type

```
cat2ds9 --h
```

With the help of these two commands we extract the list of found sources to the region file **found.reg** and sources from the catalog to the region file **cat.reg**

With the help of **ds9** you can see several images at once. For example if you want to see the same energy band with in two ways - one with found sources and one with the catalog ones

```
ds9 jmx2_sky_ima.fits\[2] jmx2_sky_ima.fits\[2]
```

You can zoom images choosing 'Zoom In' from the Zoom menu and load the regions created above from the Region menu. In the Figure 10 the left image shows the Crab region in the first energy band with the catalog sources, and the right one - the same region with the found sources (Science Window 010200210010). Only Crab was found.

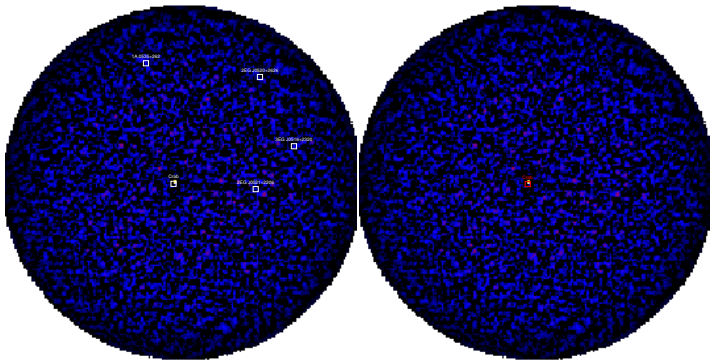

Figure 10: Crab region. On the left image catalog sources are shown, and on the right one you see the only found source.

7.3.2 Case 2: Weak Sources

During the analysis we have used the default value of the minimum detection level for the source acceptance (**Warning**: It is NOT a statistical sigma!, see discussion in Section 8.7.2):

```
IMA_minDetLev=20
```

You can play a bit with this parameter, its decreasing leads to the increase of the found source number, but the significance of these sources will be low and some of these new found sources could be spurious. However, currently the only chance to detect weak sources is setting `IMA_minDetLev` to less then 20.

Let us repeat the analysis with a new minimum source detection level:

```
cd $REP_BASE_PROD
og_create idxSwg=jemx2.lst ogid=crab_12  baseDir="./" instrument=JMX2
cd obs/crab_12
jemx_science_analysis startLevel="CAT_I" endLevel="IMA"  \
                      IMA_minDetLev="12" IMA_vignCorr=no jemxNum=2
```

Checking the result for e.g. Science Window `010200210010`

```
fv scw/010200210010.000/jmx2_srcl_res.fits
```

we notice that besides the Crab seven new sources were found. These sources are close to the edge, and you should be very careful with such sources. To verify whether the new source is a real one you can start with a simple statistic analysis with the help of **ds9**.

Draw the slice (in **ds9** you choose **region**, then **projection**) through the source position (see Figure 11) and look on the result. Root mean square of the background value around the source give a first impression of the noise amplitude.

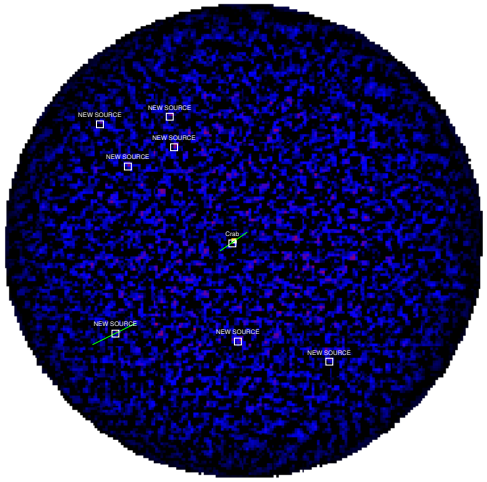

Figure 11: Illustration for Case 2, see text

In Figure 12 you see two such slices for Crab and one of new sources. Crab is clearly above the background, while the new source is compatible with the background and most probably is not a real one.

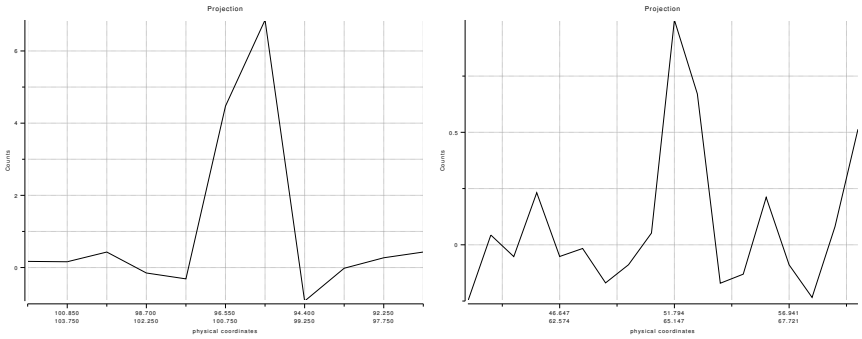

Figure 12: Left: Comparison between Crab flux and surrounding background. **Right:**The same for the new source.

7.3.3 Case 3: Bright Sources at the edge of the field of view

Experience has shown that there are mainly spurious sources at the offset angle bigger than five degrees. To avoid the detection of such sources the default settings of the script limit the radius where the sources are looked for to `IMA_angleLimit=5.` However in the case you have a bright source close to the edge of the field of view you may want to increase this parameter in order to force the software to analyze this source. Note however, that at the moment any flux extraction of the source too close to the edge is less reliable than the one for the source in the FCFOV.

7.3.4 Case 4: Vignetting correction

The presence of the collimator introduces a vignetting of off-axis sources, see Section 8.7.3 for a discussion. In the previous examples we run the analysis for the whole field of view, without taking

the vignetting correction into account.

```
IMA_vignCorr=no
```

In the current example, we are applying a vignetting correction with a minimum vignetting factor of 0.01.

```
IMA_threshold=0.01
```

This means that only pixels in the sky image for which at least 1% of the original flux reaches the detector are corrected for vignetting (this means division by the vignetting factor), while pixels with even less transmitted flux are set to "empty" values.

```
cd $REP_BASE_PROD
og_create idxSwg=jemx2.lst ogid=crab_vign01  baseDir="./" instrument=JMX2
cd obs/crab_vign01
jemx_science_analysis startLevel="CAT_I" endLevel="IMA"\
                      IMA_minDetLev=15 jemxNum=2\
                      IMA_vignCorr=y IMA_threshold=0.01
```

Setting this value to a higher value will give us a less noisy image in the border but a smaller image than before. If you want only to get an image of the fully coded field of view region, set IMA_threshold to 0.63.

```
cd ../..
og_create idxSwg=jemx2.lst ogid=crab_vign63  baseDir="./" instrument=JMX2
cd obs/crab_vign63
jemx_science_analysis startLevel="CAT_I" endLevel="IMA"
                      IMA_minDetLev=15\ jemxNum=2\
                      IMA_vignCorr=y IMA_threshold=0.63
```

Notice that now you may have sources found outside the image. It happens due to the fact that sources are looked for in the full field of view within the IMA_angleLimit, before the image was cut.

7.3.5 Case 5: IMA 2 level

Initially IMA2 level was planned to produce a mosaic image. At the moment mosaicking of the pointings with different pointing directions does not improve the results, as a systematic noise at the rim of the individual images is summed up with the centers of other images. Thus OSA 4.2 pipeline do not produce any mosaic image. For the staring case it can be done manually with *image_mosaic*. The situation will be improved in OSA 5.

The only thing that is done at IMA2 level at the moment is a collection of the results from the individual science windows. If you run

```
cd ../crab
jemx_science_analysis startLevel="IMA2" endLevel="IMA2"  jemxNum=2
```

in the file `jmx2_obs.-res.fits` you find the summary information on all the sources found during the analysis per Science Window. Note that as the software was looking for Crab on its own you find in this file several lines with slightly different Crab position. If you would like to use instead the catalog position, set `IMA_useCatPos=y`.

7.4 Source Spectra Extraction

7.4.1 Individual Science Windows Spectra

Let us create the spectra of the Crab. Parameter

```
SPE_timeStep=0.
```

defines the integration time in seconds for the output spectra. The default value 0. means that all data are integrated together. If the integration time is chosen to be smaller then the length of the Science Window then several sets of spectra are produced.

```
cd ../crab_vign01
jemx_science_analysis startLevel="SPE" endLevel="SPE" jemxNum=2
```

The results of the spectral analysis data are in the file

```
 scw/RRRRPPPPSSSF/jmx2_srcl_spe.fits
```

Look on the result of the spectral analysis of the Science Window 010200210010

```
fv scw/010200210010.000/jmx2_srcl_spe.fits
```

In this file you find four spectra, one per each source that was found. Note that the correspondence between source name and source ID can be found in file **jmx2_srcl_res.fits**.

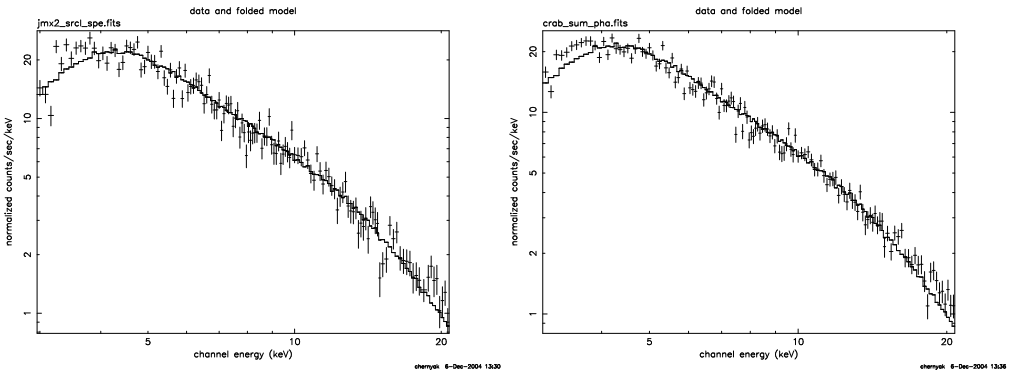

Figure 13: Left panel: Crab spectrum in ScW 010200210010, first energy band
Right panel: Combined Crab spectrum of ScW 010200210010 and ScW 010200220010, first energy band

To analyze Crab with XSPEC give the following commands:

```
cd  scw/010200210010.001/
xspec
XSPEC>cpd /xs
XSPEC>data jmx2_srcl_spe.fits{1}
XSPEC>setplot energy
XSPEC>ign **-3.0
XSPEC>ign 21.-**
XSPEC>setplot reb 5 5
```

```
XSPEC>plot ldat
XSPEC>model wabs po
XSPEC>fit
XSPEC>plot ldat
```

The result is shown in the Figure 13

Warning! Please note that if your analysis ends with a really weird looking spectrum it can be related to the problem of gain coefficients modelling. See Section 8.1.1 for a discussion.

7.4.2 Combining Spectra of different Science Windows

With the help of the **spe_pick** program, described in the Introduction to the *INTEGRAL* Data Analysis [1] it is possible to combine the spectra from the different Science Windows. To define the source for which you want to combine the spectra you should either input its Source Id, or his coordinates. To combine all the spectra belonging to the given Observation Group of the source with a given Source Id give the command:

```
spe_pick group="og_jmx2.fits[1]" instrument="JMX2"\
         source="J053432.0+220052" rootname="crab" sum=y
```

As a result four files were created:

```
crab_single_pha2.fits   All individual spectra of the source.
crab_single_arf2.fits     Corresponding individual ARFs
crab_sum_pha.fits   Combined spectrum.
crab_sum_arf.fits   ARF for the combined spectrum.
```

The resulting spectrum (which was created by XSPEC according to the procedure described in 7.4.1) is shown in right panel of Figure 13.

The possibility to specify the source by its coordinates is very useful in the case of new sources. For the one of the new sources found in the ScW 010200210010:

```
spe_pick group="og_jmx2.fits[1]" instrument="JMX2"\
         source="none" rootname="new" sum=y coor_sys="fk5"\
 ra_obj="8.3460121E+01" dec_obj="1.9374439E+01" radius=0.1
```

It is also possible to combine the spectra of the Science Windows which belong to different observation groups. In order to do that you should with the help of the **txt2idx** program (see [1] for a description) create an index which will contain all the desired Science Windows. To create such an index you should first make a list of all the science window groups which spectra you want to sum up. In the example below we create file LIST.txt with two lines:

```
scw/010200210010.000/swg_jmx2.fits[1]
scw/010200220010.000/swg_jmx2.fits[1]
```

With the help of this file you can create an index, and then run *spe_pick*:

```
txt2idx index=jmx2speidx.fits template=GNRL-SCWG-GRP-IDX.tpl element=LIST.txt
spe_pick jmx2speidx.fits\[1] instrument=JMX2 source=J053432.0+220052 \
rootname=crab sum=y
```

7.5 Source Lightcurve Extraction

7.5.1 Individual Science Windows Lightcurves

To set the binning time for the light curve extraction you should use the parameter

```
LCR_timeStep=10.
```

which gives the length of the time bin in seconds.

To start the analysis give the following command:

```
jemx_science_analysis startLevel="LCR" endLevel="LCR" \
                      jemxNum=2  LCR_timeStep=100.
```

As a result for each found source a lightcurve is produced at each energy band. The results are written to the file

```
scw/RRRRPPPPSSSF.000/jmx2_src_lc.fits
```

7.5.2 Combining Lightcurves from Different Science Windows

Similar to the spectral case there is a tool **lc_pick** (see [1] for details) to combine the lightcurves from the different Science Windows.

```
lc_pick group="og_jmx2.fits[1]" source="J053432.0+220052"\
        lc="crab_lc.fits" merge=y lcselect="CHANMIN==46"
```

The resulting lightcurve is shown in Figure 14.

You can also build a lightcurve of a new source by leaving the `source=""` and specifying instead the source coordinates.

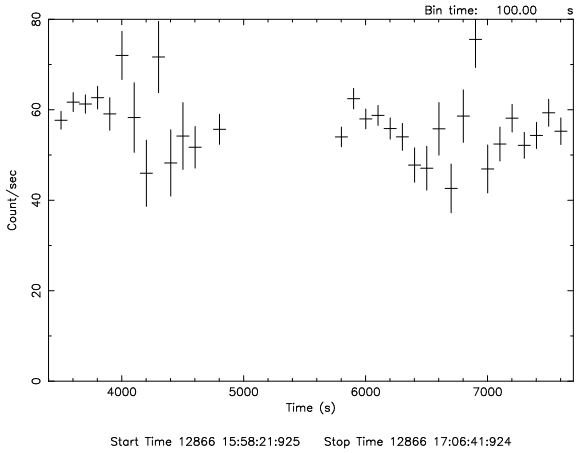

Figure 14: Crab lightcurve, first energy band

It is also possible to sum up lightcurves from different observation groups. The method to do it is the same as in spectral case.

The vignetting by the collimator and mask support structure of JEM-X has a more complex structure than originally thought. Work is ongoing to calibrate this effect but has not yet finished. Therefore, source fluxes can jump significantly, on the order of 10%, from one Science Window to the next. At off-axis angles of 5 degrees this can even reach 30% in bad cases. This flux changes affect the whole spectral range, so spectral shapes are less affected.

7.6 User GTIs

The way of creating User Good Time Intervals is described in the Introduction to the *INTEGRAL* Data Analysis [1]. To use your own GTI within the JEM-X analysis you should set two parameters – `GTI_gtiUser`, defining the location of your file, and `GTI_TimeFormat` defining the time format of the user GTI table. The possible values of the `GTI_TimeFormat` are `IJD` for the Integral Julian Date (see Introduction to the *INTEGRAL* Data Analysis [1], `UTC` and `OBT`. Below you find an example of the command to launch the JEMX analysis with the default values using the user GTI table **user_gti.fits**

```
jemx_science_analysis startLevel="GTI" endLevel="IMA" \
                      COR_outputExists=y \
                      DEAD_outputExists=n \
                      GTI_gtiUser="userdata/user_gti.fits[1]" \
                      GTI_TimeFormat="IJD"
```

7.7 User catalog

Even if the source is too weak to be detected by the software, you still can extract have all the results referring to a given sky position. To do that you should create a user catalog with the same format as in general reference catalog (see corresponding Section in [1]). The easiest way to create your user catalog is to copy to your own directory the general reference catalog

```
cp ibis_data_rep/cat/hec/gnrl_refr_cat_0009.fits   ibis_data_rep/user_cat.fits
```

and to delete all the sources you are not interested in. For the rest ones you should change the value in the **FLAG** column to 1. You can also add rows with the sources that are not in the catalog. The columns that you have to fill are **SOURCE_ID**, **NAME**, **RA_OBJ**, **DEC_OBJ** and **FLAG**. For **SOURCE_ID** you can put anything you what, providing that the combination you enter is unique. Coordinates **RA_OBJ** and **DEC_OBJ** should be in J2000, degrees. The **FLAG** column should be filled with 1.

Note that for the sources with FLAG 1 the position is taken directly from the catalog, without any following modification.

To use your catalog in the analysis you should set the parameter **CAT_I_usrCat**:

```
jemx_science_analysis   CAT_I_usrCat="../../user_cat.fits[1]"\
                        IMA_useCatPos=y
```

7.8 Radius Limit

The particle background in the JEM-X detectors rises sharply towards the rim. Currently it cannot be modeled precisely. In addition, the four calibration sources are located in the detector rim. Though the calibration photons are mostly recognized and taken out on-board, some will contribute to the measured flux. To avoid these critical areas there is a parameter `radiusLimit`

which reduce the detector area under consideration. The default value was set to 105, see Figure 15 for details.

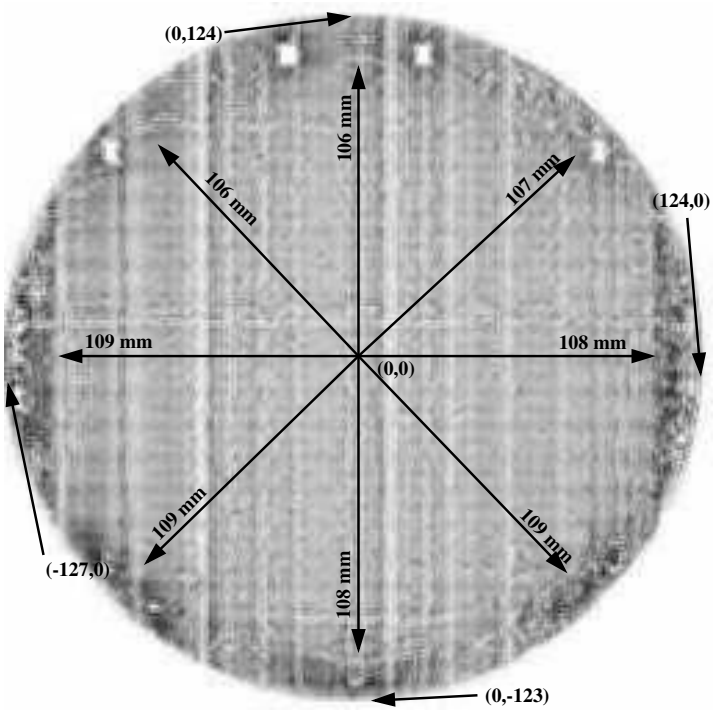

Figure 15: Shadowgram of JEM-X 2 from a background observation. The detector image has been smoothed to better show the large scale structure with the increased background at the rim and the degraded anode sections. At the top the areas of the calibration sources are visible as square areas slightly distorted by the smoothing.

7.9 Images with fine resolution

It possible to create images with fine resolution. To do this set the parameter `IMA_fineResol` to `y`, as in the following example. At the moment fine resolution images are not used in the pipeline for any flux extraction, and even no source search is performed.

```
og_create idxSwg=jemx2.lst ogid=crab_fine  baseDir="./" instrument=JMX2
cd obs/crab_fine
jemx_science_analysis startLevel="COR" endLevel="IMA" \
BIN_I_shdType=1 IMA_fineResol=y
```

The example of the image of the Crab region with fine resolution is given on the Figure 16. It was created with the command:

```
ds9 scw/010200210010.000/jmx2_sky_ima.fits -cmap b -scale sqrt -scale limits 0 30
```

7.10 Calibration Instances

There has been a small number of instrument configuration updates such as changes in the event rejection criteria that have led to changes in the responses, in particular at low energy. The

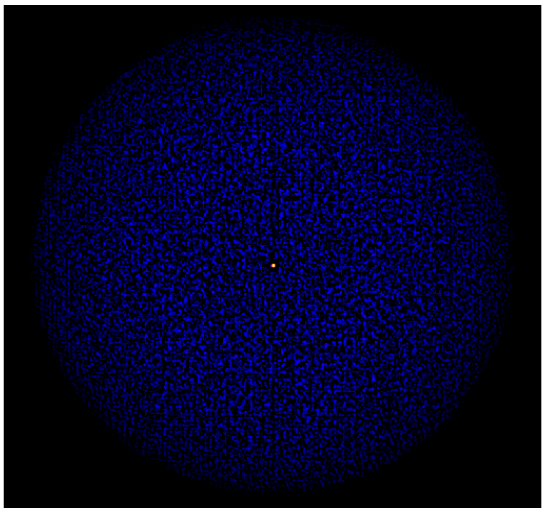

Figure 16: Fine resolved image of the Crab region

calibration periods span between such updates, except the dividing between period 4 and 5 which is artificial. A calibration using the Crab Nebula defines the response in each period except in the very beginning of the INTEGRAL mission where no good calibration can be done. The time limits for the periods are given in the table below. The three rightmost columns define the instance numbers of the RMF IC files to use in a given period and a given version of *j_src_spectra*. With OSA4 version 4.1.0 and RMF instances 18 – 23 are supplied.

Table 5: Instance number to use

Cal period	IJD interval		j_src_spectra		
	JMX1	JMX2	3.5.1	4.0.0	4.1.0
1	1030.17 – 1043.33	1030.17 – 1046.33	6	12	18
2	1043.33 – 1059.33	1046.33 – 1059.33	7	13	19
3	1059.33 – 1151.29	1059.33 – 1151.29	8	14	20
4	1151.29 – 1237.70	1151.29 – 1237.70	9	15	21
5	1237.70 – 1507.50	1237.70 – 1426.10	10	16	22
6	1507.50 – ?	1426.10 – 1536.50	11	17	23

7.11 More Examples

More examples can be found in the program of the hands-on session of the 1st *INTEGRAL* Data Analysis Workshop http://isdc.unige.ch/ chernyak/hand-on.html The viewgraphs of the oral presentations can be found at http://isdc.unige.ch/index.cgi?Science+workshop+Science/workshop/timetable.html

Table 6: *jemx_science_analysis* parameters description

Name	Type	Description
ogDOL	string	DOL of the Observational Group to be analyzed. default: “”
jemxNum	integer	JEM-X instrument number (1 or 2) default: `2`
startLevel	string	Analysis level at which analysis begins. The names of the possible analysis levels are listed in the table 4 **default**: “`CAT_I`”
endLevel	string	Analysis level at which analysis finishes. The names of the possible analysis levels are listed in the table 4. default: “`IMA2`”
COR_outputExists	boolean	Assume already existing output default: “`n`”
DEAD_outputExists	boolean	Assume already existing output default: “`n`”
skipLevels	string	Analysis levels to be skipped (use with caution!) default: “`BKG,LCR,BIN_T`”
chatter	integer	Verbosity level possible values: `0` – `5` `2` – normal default: `2`
clobber	boolean	Clobber existing output data? default: `y`
osimData	boolean	Input data was created by ISDC simulator? default: `n`
ignoreScwErrors	boolean	Ignore all SW processing errors? default: `n`
Parameters copied to several binning data tasks		
nChanBins	integer	Number of bands for shadowgrams and lightcurves possible values: `1` – `100` default: `4`
chanLow	string	Lower channel boundaries for shadowgrams and lightcurves default: “`46 83 129 160`”
chanHigh	string	Upper channel boundaries for shadowgrams and lightcurves default: “`82 128 159 223`”
timeStart	real	Start of time interval [IJD] `-1` – use Science Window bounds default: `-1`
timeStop	real	End of time interval [IJD] `-1` – use Science Window bounds default: `-1`

nPhaseBins	integer	Number of phase bins (N<0 = abs(N) equally spaced bins) default: `0`
phaseBins	string	Phase bin sizes, separated by space default:
radiusLimit	real	Use events within this detector radius [mm] possible values: `0.0` –`130.0` default: `105.0`
Parameters required for Instrument Characteristics selection		
IC_Group	string	DOL of the Instrument Characteristics master group. This group is accessed by the script to find the calibration data relevant for the current Science Window. default: "`../../idx/ic/ic_master_file.fits[GROUPING,1]`"
IC_Alias	string	Selection alias for Instrument Characteristics. By changing this alias different instances of IC data can be selected. default: "`CONS`"
instMod	string	DOL of JEM-X Instrument Model Group (empty=find in IC) default:
response	string	Filename of standard RMF and ARF (empty=find in IC) default:
Parameters specific to corrections (**COR**)		
COR_gainHist	string	DOL of the Index Group with gain variation history. This data is stored per revolution and thus not accessible via the IC system. default: ""
COR_gainModel	integer	Gain history smoothing model to be applied possible values: `0` Linear interpolation between gain history values, `1` Fixed gain parameters are used - this is the emergency solution when any part of data read in or processing fails. `2` Exponential gain decay with linear segment immediately after switch. Models normal time variation of gain slope in a revolution default: `2`
Parameters specific to Good Time Intervals (**GTI**)		
GTI_gtiUser	string	DOL of the input user GTI default: " "
GTI_TimeFormat	string	Time format to be used possible values: "`IJD`", "`UTC`", "`OBT`" default: "`IJD`"
GTI_BTI_Dol	string	DOL of a bad time interval table. default: " "

GTI_BTI_Names	string	Input Bad Time Interval names to be considered default: " "
GTI_attTolerance	real	Accepted attitude variability [arc min] default: `0.5`
GTI_limitTable	string	DOL of table with parameter limits default: ""
GTI_gtiJemxNames	string	Names of instrumental GTIs to be included in merged GTI default: ""
GTI_gtiScNames	string	Names of spacecraft GTIs to be included in merged GTI default: ""
GTI_MergedName	string	Name of merged GTI to be used in analysis default: "`MERGED`"
GTI_Accuracy	string	Used accuracy for OBT to IJD conversion and vice versa possible values: "`any`", "`inaccurate`", "`accurate`" default: "`any`"
Parameters specific to catalog extraction (**CAT_I**)		
CAT_I_refCat	string	DOL of the Reference Catalog default: "`$ISDC_REF_CAT`"
CAT_I_usrCat	string	DOL of the User Catalog. Currently not used. default: "" ""
CAT_I_radiusMin	string	Low limit for the position selection. Can be multiple limits with separating blank default: "`0 2.4`"
CAT_I_radiusMax	string	High limit for the position selection. Can be multiple limits with separating blank default: "`2.4 6.6`"
CAT_I_fluxDef	string	Column used for flux selection. default: "`0`"
CAT_I_fluxMin	string	Low limit for flux selection. default: ""
CAT_I_fluxMax	string	High limit for flux selection. default: ""
CAT_I_class	string	Object class of sources to select default: ""
CAT_I_date	real	IJD for the public data. possible values: <0 – all public; 0 – all private; >0 – according to DAY_ID default: "`-1`"
Parameters specific to background modeling (**BKG**)		

BKG_simulated	boolean	Use simulated background models default: `n`
Parameters specific to shadowgram binning (**BIN_I**)		
BIN_I_evtType	integer	Event type possible values: `0` – FULL, `1` – REST, `-1` – both default: `-1`
BIN_I_backCorr	boolean	Perform background correction? default: `n`
BIN_I_shdType	integer	Type of shadowgram possible values: `1` – standard, `2` – raw-standard `3` – regular default: `3`
BIN_I_shdRes	string	DOL of the output shadowgrams default:
BIN_I_rowSelect	string	CFITSIO selection string on events default: " "
BIN_I_gtiNames	string	Names of GTI tables to be used default: " "
Parameters specific to imaging (**IMA**)		
IMA_minDetLev	real	Minimum detections level for source acceptance possible values: `5.` – `100.` default: `20`
IMA_vign Corr	boolean	Correct for vignetting? default: `no`
IMA_threshold	real	Vignetting lower limit default: `0.01`
IMA_angleLimit	real	Maximum offset for source acceptance [deg] possible values: `0.` – `6.6` default: `5.`
IMA_useCatPos	boolean	Flag for catalog position to override found position default: "y"
IMA_ignoreAnode	string	Anode numbers (up to four numbers) to ignore default: ""
IMA_numPixelSubDiv	integer	Number of pixel subdivisions possible values: `1` – `500` default: `20`
IMA_fineResol	boolean	Create also sky images with fine resolution (slow)? default: `n`

IMA_dimImage	integer	Dimension of fine resolved sky image possible values: `0` – `825` default: `0`
IMA_maxNumTrials	integer	Maximum number of trials in the source search default: `20`
IMA_minDist	real	Minimum source separation [arcmin] default: `4.`
IMA_relDist	real	Maximally allowed value for reldist default: `1.5`
IMA_fluxLimit	real	Lower flux limit for alerts of unfound sources [Counts/cm/s^2] default: `0.0`
IMA_searchRad	real	Range of search grid around nominal found source positions default: `0.25`
IMA_gridNum	integer	Number of grid steps on one side of search grid default: `25`
IMA_distFuzz	real	"Fuzz" allowed in relative distances default: `0.15`
Parameters specific to source spectra extraction (**SPE**)		
SPE_timeStep	real	Binning time for spectra in seconds (`0.0` – bin all data together). default: `0.0`
SPE_vignCorr	boolean	Correct for vignetting? default: `y`
SPE_bgrMethod	integer	Background subtraction method possible values: `0` – Flat, `1` – Model default: `0`
SPE_evtType	integer	Event type (0=FULL, 1=REST, -1=both) possible values: `0` – FULL, `1` – REST, `-1` – both default: `-1`
SPE_precisionLevel	integer	Speed - precision level, see more details in Section 8.8.1 possible values: `0` – basic approach `20` – more detailed approach default: `20`
SPE_fluxScaling	integer	Flux scaling to area possible values: `1` – Full area open to the illumination `2` – 100cm^2 `3` – 1cm^2 default: `2`

SPE_skipNearDeadAnode	boolean	Ignore pixels near dead anodes? default: `y`
SPE_skipHotSpot	boolean	Ignore pixels in hotspot area? default: `n`
SPE_tAccuracy	integer	Time Correlation accuracy possible values: `0` – high, `1` – low, `3` – any default: `3`
SPE_rowSelect	string	CFITSIO selection string on events default: " "
SPE_useRaDec	boolean	Use sky coordinates (Ra,Dec) instead of instrument coordinates? default: `y`
Parameters specific to source lightcurve extraction (LCR)		
LCR_timeStep	real	Binning time for spectra in seconds, negatoive value means that time bin is equal to the science window exposure. default: `10.0`
LCR_vignCorr	boolean	Correct for vignetting? default: `y`
LCR_bgrMethod	integer	Background subtraction method possible values: `0` – Flat, `1` – Model default: `0`
LCR_evtType	integer	Event type (0=FULL, 1=REST, -1=both) possible values: `0` – FULL, `1` – REST, `-1` – both default: `-1`
LCR_precisionLevel	integer	Speed - precision level, see more details in Section 8.8.1 possible values: `0` – basic approach, `20` – more detailed approach default: `20`
LCR_fluxScaling	integer	Flux scaling to area possible values: `1` – Full area open to the illumination `2` – 100cm^2 `3` – 1cm^2 default: `2`
LCR_skipNearDeadAnode	boolean	Ignore pixels near dead anodes? default: `y`
LCR_skipHotSpot	boolean	Ignore pixels in hotspot area? default: `n`

LCR_tAccuracy	integer	Time Correlation accuracy possible values: `0` – high, `1` – low, `3` – any default: `3`
LCR_rowSelect	string	CFITSIO selection string on events default: " "
LCR_useRaDec	boolean	Use sky coordinates (Ra,Dec) instead of instrument coordinates? default: `y`
Parameters specific to detector spectra binning (**BIN_S**)		
BIN_S_rowSelectEvts	string	CFITSIO selection string on events default: ""
BIN_S_rowSelectSpec	string	CFITSIO selection string on spectrum mode data default: ""
BIN_S_evtType	integer	Data format to bin possible values: `-1` – all, `0` – FULL, `1` – REST, `2` – SPTI, `4` – SPEC default: `-1`
Parameters specific to detector lightcurve binning (BIN_T)		
BIN_T_rowSelect	string	CFITSIO selection string on events default: ""
BIN_T_evtType	integer	Data format to bin possible values: `-1` – all, `0` – FULL, `1` – REST, `2` – SPTI, `4` – SPEC default: `-1`
Parameters specific to *jemx_obs_analysis* (IMA_2)		
IMA2_mosaicselection	string	Selection string for input image filtering default: ""
IMA2_mosaicFileDOL	string	DOL of the output image mosaic File default:
IMA2_srcFileDOL	string	DOL of the output source list mosaic default:
IMA2_srcselect	string	CFITSIO selection string applied to input tables default:

IMA2_srcattach	boolean	Attach resulting table to group? default: `y`